Docket N .: PF-0636 USN

IN THE CLAIMS

This listing of the claims replaces all prior versions of the claims in the application.

1-20. (Canceled)

21. (Previously Presented) An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:12,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:12, wherein said polypeptide binds to human immunodeficiency virus glycoprotein gp120, and

c) a biologically active fragment of a polypeptide having the amino acid sequence of SEQ ID NO:12, wherein said fragment binds to human immunodeficiency virus glycoprotein gp120.

22. (Previously Presented) An isolated polypeptide of claim 21 comprising the amino acid sequence of SEQ ID NO:12.

23. (Previously Presented) An isolated polynucleotide encoding a polypeptide of claim 21.

24. (Previously Presented) An isolated polynucleotide encoding a polypeptide of claim 22.

25. (Previously Presented) An isolated polynucleotide of claim 24 comprising a polynucleotide sequence of SEQ ID NO:25.

26. (Previously Presented) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 23.

27. (Previously Presented) A cell transformed with a recombinant polynucleotide of claim 26.

28. (Previously Presented) A method of producing a polypeptide of claim 21, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 21, and

b) recovering the polypeptide so expressed.

29. (Previously Presented) A method of claim 28, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:12.

30. (Previously Presented) An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:25,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:25,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

31. (Canceled)

32. (Withdrawn) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 30, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under

conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

33. (Withdrawn) A method of claim 32, wherein the probe comprises at least 60 contiguous nucleotides.

34. (Withdrawn) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 30, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

35. (Previously Presented) A composition comprising a polypeptide of claim 21 and a pharmaceutically acceptable excipient.

36. (Previously Presented) A composition of claim 35, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:12.

37. (Previously Presented) A method for treating a disease or condition associated with decreased expression of functional HCSRP, comprising administering to a patient in need of such treatment the composition of claim 35.

38. (Withdrawn) A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 21, the method comprising:

a) exposing a sample comprising a polypeptide of claim 21 to a compound, and

b) detecting antagonist activity in the sample.

39. (Withdrawn) A method of screening for a compound that specifically binds to the polypeptide of claim 21, the method comprising:

a) combining the polypeptide of claim 21 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 21 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 21.

40. (Withdrawn) A method of screening for a compound that modulates the activity of the polypeptide of claim 21, the method comprising:

a) combining the polypeptide of claim 21 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 21,

b) assessing the activity of the polypeptide of claim 21 in the presence of the test compound, and

c) comparing the activity of the polypeptide of claim 21 in the presence of the test compound with the activity of the polypeptide of claim 21 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 21 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 21.

41. (Withdrawn) A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 25, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

42. (Withdrawn) A method of assessing toxicity of a test compound, the method comprising:

a) treating a biological sample containing nucleic acids with the test compound,

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 30 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 30 or fragment thereof,

c) quantifying the amount of hybridization complex, and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.